

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/051,644 D
Source: FW/6
Date Processed by STIC: 1-26-85

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 01/26/2005

PATENT APPLICATION: US/10/051,644D

TIME: 16:31:59

Input Set : A:\Cambria-0012.ST25.txt

Output Set: N:\CRF4\01262005\J051644D.raw

3 <110> APPLICANT: Liu, et al.,
 5 <120> TITLE OF INVENTION: Screens and Assays for Agents Useful in Controlling
 Parasitic

6 Nematodes

8 <130> FILE REFERENCE: 2002630-0012

10 <140> CURRENT APPLICATION NUMBER: 10/051,644D

11 <141> CURRENT FILING DATE: 2002-01-18

13 <160> NUMBER OF SEQ ID NOS: 33

15 <170> SOFTWARE: PatentIn version 3.2

17 <210> SEQ ID NO: 1

18 <211> LENGTH: 425

19 <212> TYPE: PRT

20 <213> ORGANISM: Artificial

22 <220> FEATURE:

23 <223> OTHER INFORMATION: Caenorhabditis elegans

25 <400> SEQUENCE: 1

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28 1          5          10          15
31 Val Ala Gln Thr Phe Gly Cys Ser Asn Thr Lys Ile Asn Asp Gln Ala
32          20          25          30
35 Arg Lys Met Phe Tyr Asp Ala His Asn Asp Ala Arg Arg Ser Met Ala
36          35          40          45
39 Lys Gly Leu Glu Pro Asn Lys Cys Gly Leu Leu Ser Gly Gly Lys Asn
40          50          55          60
43 Val Tyr Glu Leu Asn Trp Asp Cys Glu Met Glu Ala Lys Ala Gln Glu
44 65          70          75          80
47 Trp Ala Asp Gly Cys Pro Ser Ser Phe Gln Thr Phe Asp Pro Thr Trp
48          85          90          95
51 Gly Gln Asn Tyr Ala Thr Tyr Met Gly Ser Ile Ala Asp Pro Leu Pro
52          100         105         110
55 Tyr Ala Ser Met Ala Val Asn Gly Trp Trp Ser Glu Ile Arg Thr Val
56          115         120         125
59 Gly Leu Thr Asp Pro Asp Asn Lys Tyr Thr Asn Ser Ala Met Phe Arg
60          130         135         140
63 Phe Ala Asn Met Ala Asn Gly Lys Ala Ser Ala Phe Gly Cys Ala Tyr
64 145         150         155         160
67 Ala Leu Cys Ala Gly Lys Leu Ser Ile Asn Cys Ile Tyr Asn Lys Ile
68          165         170         175
71 Gly Tyr Met Thr Asn Ala Ile Ile Tyr Glu Lys Gly Asp Ala Cys Thr
72          180         185         190
75 Ser Asp Ala Glu Cys Thr Thr Tyr Ser Asp Ser Gln Cys Lys Asn Gly
76          195         200         205
79 Leu Cys Tyr Lys Ala Pro Gln Ala Pro Val Val Glu Thr Phe Thr Met
80          210         215         220

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83 Cys Pro Ser Val Thr Asp Gln Ser Asp Gln Ala Arg Gln Asn Phe Leu
 84 225 230 235 240
 87 Asp Thr His Asn Lys Leu Arg Thr Ser Leu Ala Lys Gly Leu Glu Ala
 88 245 250 255
 91 Asp Gly Ile Ala Ala Gly Ala Phe Ala Pro Met Ala Lys Gln Met Pro
 92 260 265 270
 95 Lys Leu Val Lys Tyr Ser Cys Thr Val Glu Ala Asn Ala Arg Thr Trp
 96 275 280 285
 99 Ala Lys Gly Cys Leu Tyr Gln His Ser Thr Ser Ala Gln Arg Pro Gly
 100 290 295 300
 103 Leu Gly Glu Asn Leu Tyr Met Ile Ser Ile Asn Asn Met Pro Lys Ile
 104 305 310 315 320
 107 Gln Thr Ala Glu Asp Ser Ser Lys Ala Trp Trp Ser Glu Leu Lys Asp
 108 325 330 335
 111 Phe Gly Val Gly Ser Asp Asn Ile Leu Thr Gln Ala Val Phe Asp Arg
 112 340 345 350
 115 Gly Val Gly His Tyr Thr Gln Met Ala Trp Glu Gly Thr Thr Glu Ile
 116 355 360 365
 119 Gly Cys Phe Val Glu Asn Cys Pro Thr Phe Thr Tyr Ser Val Cys Gln
 120 370 375 380
 123 Tyr Gly Pro Ala Gly Asn Tyr Met Asn Gln Leu Ile Tyr Thr Lys Gly
 124 385 390 395 400
 127 Ser Pro Cys Thr Ala Asp Ala Asp Cys Pro Gly Thr Gln Thr Cys Ser
 128 405 410 415
 131 Val Ala Glu Ala Leu Cys Val Ile Pro
 132 420 425

135 <210> SEQ ID NO: 2

136 <211> LENGTH: 1341

137 <212> TYPE: DNA

138 <213> ORGANISM: Artificial

140 <220> FEATURE:

141 <223> OTHER INFORMATION: Caenorhabditis elegans

143 <400> SEQUENCE: 2

144	atggcggtat	tagcagtggt	actacttcta	gcatgcctgg	agagagcggt	tgcacagacg	60
146	ttcggctgct	ctaacaccaa	gatcaatgac	caggctcgta	agatgttcta	tgatgctcac	120
148	aatgatgcaa	gacgaagcat	ggctaaagg	cttgagccaa	acaagtgcgg	actcttatct	180
150	ggtggaaaga	atgtttatga	attgaattgg	gattgcgaga	tggaagcaaa	agctcaggaa	240
152	tgggcagacg	gatgtcccag	ctctttccag	acatttgatc	caacatgggg	gcagaactac	300
154	gcgacgtaca	tgggatcgat	tgctgatccg	cttccatacg	cttccatggc	tggttaatggg	360
156	tggtggtcgg	aaattagaac	cgtaggactt	acggatcctg	ataacaagta	cactaacagt	420
158	gcaatgttcc	gatttgctaa	tatggcaaat	ggtaaagctt	cagcttttgg	atgtgcatac	480
160	gcgttgtgcg	caggaaaact	atccatcaat	tgcatttaca	acaagatagg	atacatgacc	540
162	aatgctatca	tttatgaaaa	aggagatgcc	tgtaccagtg	acgctgaatg	caccacctac	600
164	tcagactcac	aatgcaaaaa	cggctcttgc	tataaggcac	ctcaagctcc	agtcgttgag	660
166	actttcacaa	tgtgcccttc	ggtcacggac	cagtcgggatc	aggcgcgtca	aaacttcttg	720
168	gacacccata	acaaattgcy	tacaagcctt	gccaaaggac	ttgaagctga	tggaattgcc	780
170	gctggagcat	ttgcaccaat	ggccaagcaa	atgccaaaac	tggtaaaata	cagctgcaca	840
172	gttgaagcaa	acgccagaac	atgggcacaa	ggatgccttt	accagcattc	aacaagcgca	900
174	cagagaccag	gactcgggtga	aaatctttat	atgatcagca	ttaacaacat	gcctaaaatt	960

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176 caaaccgcgg aggactcctc aaaggcttgg tgggccgagt tgaaagactt cggagtcggt 1020
178 tctgacaaca ttctgaccca agcagttttt gatcgtggcg ttggacatta cacacaaatg 1080
180 gcatgggaag gaactactga aattggatgt tttgtggaga attgtccaac attcacttat 1140
182 tccgtatgcc aatatggtcc agcgggaaac tacatgaacc aactaatcta taccaagggc 1200
184 tcaccatgca cagctgacgc cgattgcccga ggaaccacaga catgcagtgt cgctgaagca 1260
186 ttatgtgtta tcccttagta aattttctat gcaactcttt gaaagtcata ataaatatgc 1320
188 aaaaattaaa aaaaaaaaaa a 1341
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 473
193 <212> TYPE: PRT
194 <213> ORGANISM: Artificial
196 <220> FEATURE:
197 <223> OTHER INFORMATION: Caenorhabditis elegans
199 <400> SEQUENCE: 3
201 Met Asn Val Val Leu Ser Ala Val Thr Leu Phe Leu Ile Phe Arg Tyr
202 1 5 10 15
205 Ala Gln Thr Val Asn Ile Glu Gly Ser Gly Gly Asn Asp Glu Leu Leu
206 20 25 30
209 Glu Gln Asn Val Trp Asn Asp Val Asp Asp Lys Val Val Glu Ala Leu
210 35 40 45
213 Gly Gly Leu Asp Asp Glu Leu Leu Thr Glu His Val Cys Asn Lys Ser
214 50 55 60
217 Thr Ile Thr Gln Leu Gln Gln Glu Ile Ile Leu Thr Thr His Asn Glu
218 65 70 75 80
221 Leu Arg Arg Ser Leu Ala Phe Gly Lys Gln Arg Asn Lys Arg Gly Leu
222 85 90 95
225 Met Asn Gly Ala Arg Asn Met Tyr Lys Leu Asp Trp Asp Cys Glu Leu
226 100 105 110
229 Ala Ser Leu Ala Ala Asn Trp Ser Thr Ser Cys Pro Gln His Phe Met
230 115 120 125
233 Pro Gln Ser Val Leu Gly Ser Asn Ala Gln Leu Phe Lys Arg Phe Tyr
234 130 135 140
237 Phe Tyr Phe Asp Gly His Asp Ser Thr Val His Met Arg Asn Ala Met
238 145 150 155 160
241 Lys Tyr Trp Trp Gln Gln Gly Glu Glu Lys Gly Asn Glu Asp Gln Lys
242 165 170 175
245 Asn Arg Phe Tyr Ala Arg Arg Asn Tyr Phe Gly Trp Ala Asn Met Ala
246 180 185 190
249 Lys Gly Lys Thr Tyr Arg Val Gly Cys Ser Tyr Ile Met Cys Gly Asp
250 195 200 205
253 Gly Glu Ser Ala Leu Phe Thr Cys Leu Tyr Asn Glu Lys Ala Gln Cys
254 210 215 220
257 Glu Lys Glu Met Ile Tyr Glu Asn Gly Lys Pro Cys Cys Glu Asp Lys
258 225 230 235 240
261 Asp Cys Phe Thr Tyr Pro Gly Ser Lys Cys Leu Val Pro Glu Gly Leu
262 245 250 255
265 Cys Gln Ala Pro Ser Met Val Lys Asp Asp Gly Gly Ser Phe Gln Cys
266 260 265 270
269 Asp Asn Ser Leu Val Ser Asp Val Thr Arg Asn Phe Thr Leu Glu Gln

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270          275          280          285
273 His Asn Phe Tyr Arg Ser Arg Leu Ala Lys Gly Phe Glu Trp Asn Gly
274          290          295          300
277 Glu Thr Asn Thr Ser Gln Pro Lys Ala Ser Gln Met Ile Lys Met Glu
278 305          310          315          320
281 Tyr Asp Cys Met Leu Glu Arg Phe Ala Gln Asn Trp Ala Asn Asn Cys
282          325          330          335
285 Val Phe Ala His Ser Ala His Tyr Glu Arg Pro Asn Gln Gly Gln Asn
286          340          345          350
289 Leu Tyr Met Ser Ser Phe Ser Asn Pro Asp Pro Arg Ser Leu Ile His
290          355          360          365
293 Thr Ala Val Glu Lys Trp Trp Gln Glu Leu Glu Glu Phe Gly Thr Pro
294          370          375          380
297 Ile Asp Asn Val Leu Thr Pro Glu Leu Trp Asp Leu Lys Gly Lys Ala
298 385          390          395          400
301 Ile Gly His Tyr Thr Gln Met Ala Trp Asp Arg Thr Tyr Arg Leu Gly
302          405          410          415
305 Cys Gly Ile Ala Asn Cys Pro Lys Met Ser Tyr Val Val Cys His Tyr
306          420          425          430
309 Gly Pro Ala Gly Asn Arg Lys Asn Asn Lys Ile Tyr Glu Ile Gly Asp
310          435          440          445
313 Pro Cys Glu Val Asp Asp Asp Cys Pro Ile Gly Thr Asp Cys Glu Lys
314          450          455          460
317 Thr Thr Ser Leu Cys Val Ile Ser Lys
318 465          470
321 <210> SEQ ID NO: 4
322 <211> LENGTH: 1422
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Caenorhabditis elegans
329 <400> SEQUENCE: 4
330 atgaacgtgg tcctttccgc tgtcactctt tttcttattt ttcgatatgc gcagactgtg      60
332 aatatagaag gcagtggagg aaatgatgag cttcttgagc agaacgtgtg gaacgatgta      120
334 gacgacaagg ttgtagaagc acttggtggt cttgatgatg aactgctaac cgaacatgtg      180
336 tgtaacaaat caacgatcac tcagctacag caggagatca tcttgacaac ccacaatgaa      240
338 ttacgaagat cattggcttt cggaaagcaa agaaacaaga gaggtctcat gaacggtgcg      300
340 agaaatatgt ataaactgga ttgggattgt gaactggcat cacttgacgc caattggtca      360
342 acctcctgcc ctcagcactt tatgccgcaa tcggtacttg gctccaacgc tcagcttttt      420
344 aagcgtttct atttttattt tgatgggcac gactctactg tacatatgcg aaacgcgatg      480
346 aagtattggt ggcagcaagg tgaagaaaaa ggcaatgagg atcagaaaaa tagattctat      540
348 gccagacgaa attatttttg atgggcaaac atggcaaaag gaaaaacata tcgagttgga      600
350 tgctcgtata ttatgtgcgg cgacggtgaa tctgcacttt tcaactgtct ttataacgaa      660
352 aaagcccaat gcgaaaaaga aatgatttac gaaaatggaa aacctgtctg tgaggataaa      720
354 gactgttttc catatccagg atcaaaatgt ttagtacctg aaggattatg tcaagcacct      780
356 tctatggtaa aggatgatgg aggaagtttc caatgtgata actcccttgt gtcagatgtc      840
358 acccgcaatt tcactttgga gcaacacaat ttttatagat ctctgtcttg aaaaggtttt      900
360 gaatggaatg gagaaacaaa cacttcccag ccaaaggcta gtcaaagat caaaatggag      960
362 tatgactgca tgttggaacg gtttgcacaa aactgggcaa ataattgcgt ttttgcacac      1020

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364 tcggcacatt acgaaagacc gaatcagggt cagaatctct acatgagttc tttctcaaac 1080
366 cctgataccta gaagccttat acatacggcc gtcgagaagt ggtggcagga attggaggag 1140
368 ttcggtactc caattgataa cgttctgaca cccgaattgt gggatttgaa agggaaaagcg 1200
370 ataggacatt acactcagat ggcttgggat cgtacttacc gtcttggttg tggaatcgca 1260
372 aactgtccga agatgtcgta cgtgggttgt cactatgggc cagcaggcaa cagaaaagaac 1320
374 aataaaatct atgaaatcgg ggatccttgc gaagtcgatg atgattgccc gattggaaca 1380
376 gattgtgaaa agacaacttc tttatgtgtg atctcaaaat aa 1422
379 <210> SEQ ID NO: 5
380 <211> LENGTH: 24
381 <212> TYPE: DNA
382 <213> ORGANISM: Artificial
384 <220> FEATURE:
385 <223> OTHER INFORMATION: Primer for Caenorhabditis elegans
387 <400> SEQUENCE: 5
388 gccaaaacaag tgcggactct tatc 24
391 <210> SEQ ID NO: 6
392 <211> LENGTH: 23
393 <212> TYPE: DNA
394 <213> ORGANISM: Artificial
396 <220> FEATURE:
397 <223> OTHER INFORMATION: Primer for Caenorhabditis elegans
399 <400> SEQUENCE: 6
400 gtgctagttt ttgacgaacc cag 23
403 <210> SEQ ID NO: 7
404 <211> LENGTH: 18
405 <212> TYPE: PRT
406 <213> ORGANISM: Artificial
408 <220> FEATURE:
409 <223> OTHER INFORMATION: Caenorhabditis elegans
411 <400> SEQUENCE: 7
413 Met Ala Val Leu Ala Val Val Leu Leu Leu Ala Cys Leu Glu Arg Ala
414 1 5 10 15
417 Val Ala
421 <210> SEQ ID NO: 8
422 <211> LENGTH: 21
423 <212> TYPE: DNA
424 <213> ORGANISM: Artificial
426 <220> FEATURE:
427 <223> OTHER INFORMATION: Primer for Caenorhabditis elegans
429 <400> SEQUENCE: 8
430 cacaatctgt tccaatcggg c 21
433 <210> SEQ ID NO: 9
434 <211> LENGTH: 21
435 <212> TYPE: DNA
436 <213> ORGANISM: Artificial
438 <220> FEATURE:
439 <223> OTHER INFORMATION: Primer for Caenorhabditis elegans
441 <400> SEQUENCE: 9
442 cgtggtcctt tccgctgtca c 21

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/051,644D

DATE: 01/26/2005
TIME: 16:32:00

Input Set : A:\Cambria-0012.ST25.txt
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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33

VERIFICATION SUMMARY

DATE: 01/26/2005

PATENT APPLICATION: US/10/051,644D

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Input Set : A:\Cambria-0012.ST25.txt

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